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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/721,404

DATE: 08/04/2004

TIME: 10:42:32

Input Set : N:\Cr3\RULE60\10721404.raw

Output Set: N:\CRF4\08042004\J721404.raw

1 <110> APPLICANT: Tamatani, Takuya
 2 Tezuka, Katsunari
 3 <120> TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
 4 ADHESION AND SIGNAL TRANSMISSION
 5 <130> FILE REFERENCE: 06501-039001
 6 <140> CURRENT APPLICATION NUMBER: US/10/721,404
 7 <141> CURRENT FILING DATE: 2003-11-25
 8 <150> PRIOR APPLICATION NUMBER: US/09/383,551
 9 <151> PRIOR FILING DATE: 1999-08-26
 10 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00837
 11 <151> PRIOR FILING DATE: 1998-02-27
 12 <150> PRIOR APPLICATION NUMBER: JAPAN 09-62290
 13 <151> PRIOR FILING DATE: 1997-02-27
 14 <150> PRIOR APPLICATION NUMBER: JAPAN 10-62217
 15 <151> PRIOR FILING DATE: 1998-02-26
 16 <160> NUMBER OF SEQ ID NOS: 26
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 600
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)...(597)
 26 <400> SEQUENCE: 1

27	atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa	48
28	Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	
29	1 5 10 15	
30	gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata	96
31	Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	
32	20 25 30	
33	ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc	144
34	Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35	35 40 45	
36	cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat	192
37	Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	
38	50 55 60	
39	ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg	240
40	Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
41	65 70 75 80	
42	aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta	288
43	Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
44	85 90 95	

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45   tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca      336
46   Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
47           100                      105                      110
48   att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg      384
49   Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
50           115                      120                      125
51   cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc      432
52   His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
53           130                      135                      140
54   ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt      480
55   Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
56   145                      150                      155                      160
57   att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct      528
58   Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
59           165                      170                      175
60   aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct      576
61   Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
62           180                      185                      190
63   aga ctc aca gat gtg acc cta taa      600
64   Arg Leu Thr Asp Val Thr Leu
65           195
67 <210> SEQ ID NO: 2
68 <211> LENGTH: 199
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
71 <400> SEQUENCE: 2
72   Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
73     1           5           10           15
74   Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
75           20           25           30
76   Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
77           35           40           45
78   Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
79           50           55           60
80   Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
81   65           70           75           80
82   Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
83           85           90           95
84   Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
85           100          105          110
86   Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
87           115          120          125
88   His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
89           130          135          140
90   Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
91   145          150          155          160
92   Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
93           165          170          175
94   Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser

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100 <211> LENGTH: 2610
101 <212> TYPE: DNA
102 <213> ORGANISM: Homo sapiens
103 <220> FEATURE:
104 <221> NAME/KEY: CDS
105 <222> LOCATION: (26)...(622)
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108                               Met Lys Ser Gly Leu Trp Tyr Phe Phe
109                               1          5
110      ctc ttc tgc ttg cgc att aaa gtt tta aca gga gaa atc aat ggt tct      100
111      Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser
112      10          15          20          25
113      gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta      148
114      Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu
115      30          35          40
116      tgc aaa tat cct gac att gtc cag caa ttt aaa atg cag ttg ctg aaa      196
117      Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys
118      45          50          55
119      ggg ggg caa ata ctc tgc gat ctc act aag aca aaa gga agt gga aac      244
120      Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn
121      60          65          70
122      aca gtg tcc att aag agt ctg aaa ttc tgc cat tct cag tta tcc aac      292
123      Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn
124      75          80          85
125      aac agt gtc tct ttt ttt cta tac aac ttg gac cat tct cat gcc aac      340
126      Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn
127      90          95          100          105
128      tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta      388
129      Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val
130      110          115          120
131      act ctt aca gga gga tat ttg cat att tat gaa tca caa ctt tgt tgc      436
132      Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys
133      125          130          135
134      cag ctg aag ttc tgg tta ccc ata gga tgt gca gcc ttt gtt gta gtc      484
135      Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val
136      140          145          150
137      tgc att ttg gga tgc ata ctt att tgt tgg ctt aca aaa aag aag tat      532
138      Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr
139      155          160          165
140      tca tcc agt gtg cac gac cct aac ggt gaa tac atg ttc atg aga gca      580
141      Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala
142      170          175          180          185
143      gtg aac aca gcc aaa aaa tct aga ctc aca gat gtg acc cta      622
144      Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu

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145		190		195			
146	taatatggaa	ctctggcacc	cagggcatgaa	gcacgttggc	cagtttttcc	caacttgaag	682
147	tgcaagattc	tcttatttcc	gggaccacgg	agagtctgac	ttaactacat	acatcttctg	742
148	ctgggtgttt	gttcaatctg	gaagaatgac	tgtatcagtc	aatgggggatt	ttaacagact	802
149	gccttgggtac	tgccgagtc	tctcaaaaca	aacacctct	tgcaaccagc	tttggagaaa	862
150	gcccagctcc	tgtgtgctca	ctgggagtg	aatccctgtc	tccacatctg	ctcctagcag	922
151	tgcacagcc	agtaaaacaa	acacatttac	aagaaaaatg	ttttaaagat	gccaggggta	982
152	ctgaatctgc	aaagcaaagt	agcagccaag	gaccagcatc	tgtccgcatt	tcactatcat	1042
153	actacctctt	ctttctgtag	gggtgagaat	tcctctttta	atcagtcaag	ggagatgctt	1102
154	caaagctggr	gctattttat	ttctgagatg	ttgatgtgaa	ctgtacatta	gtacatactc	1162
155	agtactctcc	ttcaattgct	gaaccccagt	tgacattttt	accaagactt	tagatgcttt	1222
156	cttgtgccct	caattttctt	tttaaaaata	cttctacatg	actgcttgac	agcccaacag	1282
157	ccactctcaa	tagagagcta	tgtcttacat	tctttcctct	gctgctcaat	agttttatat	1342
158	atctatgcat	acatatatac	acacatatgt	atataaaatt	cataatgaat	atatttgcct	1402
159	atattctccc	tacaagaata	tttttgctcc	agaaagacat	gttcttttct	caaattcagt	1462
160	taaaatgggt	tactttgttc	aagttagtgg	taggaaacat	tgcccgggaat	tgaaagcaaa	1522
161	tttawwtat	tatcctatct	tctaccatta	tctatgtttt	catgggtgcta	ttaattacaa	1582
162	gttttagttct	ttttgtagat	catattaaaa	ttgcaaacaa	aatcatcttt	aatggggccag	1642
163	cattctcatg	gggtagagca	gaatattcat	ttagcctgaa	agctgcagtt	actatagggt	1702
164	gctgtcagac	tatacccatg	gtgcctctgg	gcttgacagg	tcaaaatggt	ccccatcagc	1762
165	ctggagcagc	cctccagacc	tgggtggaat	tccagggttg	agagactccc	ctgagccaga	1822
166	ggccactagg	tattcttgct	cccagaggct	gaagtcaccc	tgggaatcac	agtgggtctac	1882
167	ctgcattcat	aattccagga	tctgtgaaga	gcacatatgt	gtcagggcac	aattccctct	1942
168	cataaaaacc	acacagcctg	gaaattggcc	ctggcccttc	aagatagcct	tctttagaat	2002
169	atgatttggt	tagaaagatt	cttaaatatg	tggaaatga	ttattcttag	ctggaatatt	2062
170	ttctctactt	cctgtctgca	tgcccaaggc	ttctgaagca	gccaatgtcg	atgcaacaac	2122
171	atttgtaact	ttaggtaaac	tgggattatg	ttgtagttaa	acattttgta	actgtgtgct	2182
172	tatagtttac	aagtgagacc	cgatatgtca	ttatgcatac	ttatattatc	ttaagcatgt	2242
173	gtaatgctgg	atgtgtacag	tacagtacwt	aacttgtaat	ttgaatctag	tatgggtgtc	2302
174	tgttttcagc	tgacttggac	aacctgactg	gctttgcaca	gggtgtccct	gagttgtttg	2362
175	caggtttctg	tgtgtggggt	ggggtatggg	gaggagaacc	ttcatgggtg	cccacctggc	2422
176	ctgggtgtcc	aagctgtgcc	tgcacacatc	ctcatcccaa	gcatgggaca	cctcaagatg	2482
177	aataataatt	cacaaaattt	ctgtgaaatc	aatccagtt	ttaagaggag	ccacttatca	2542
178	aagagatttt	aacagtagta	agaaggcaaa	gaataaacat	ttgatattca	gcaactgaaa	2602
179	aaaaaaaa						2610
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184	<213>	ORGANISM: Rattus norvegicus					
185	<220>	FEATURE:					
186	<221>	NAME/KEY: CDS					
187	<222>	LOCATION: (35) ... (634)					
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189	ctggagggga	agagtgcagc	tgttcctggc	agac atg aag ccc tac ttc tgc tgc			55
190				Met Lys Pro Tyr Phe Ser Cys			
191				1 5			
192	gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat						103
193	Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn						
194	10 15 20						

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195	gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag	151
196	Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln	
197	25 30 35	
198	att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg	199
199	Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu	
200	40 45 50 55	
201	ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc	247
202	Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser	
203	60 65 70	
204	gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg	295
205	Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu	
206	75 80 85	
207	tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag	343
208	Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln	
209	90 95 100	
210	ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt	391
211	Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe	
212	105 110 115	
213	caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag	439
214	Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln	
215	120 125 130 135	
216	ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt	487
217	Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe	
218	140 145 150	
219	gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa	535
220	Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys	
221	155 160 165	
222	aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc	583
223	Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe	
224	170 175 180	
225	atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc	631
226	Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr	
227	185 190 195	
228	tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttccct	684
229	Ser	
230	200	
231	gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac	744
232	tactgatacc tccttttggtg gttttgtttg tctggatcag tgactatcag tcactcggaa	804
233	tttcagcaga ctgccctggg tttgctgagt ccttttaagg caaaccctt cttatagaag	864
234	acccggctca tatgtattca acaaacagac ctccactggga tacaatccc tctttctgcg	924
235	cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa	984
236	tgccagggtg tgaatctgta aagtacacag gcagccattg accaccgtct gtccctgttt	1044
237	tttcagattc tatttttttc catagagatc agcattcctt ctagaatcag acagtagagg	1104
238	gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt	1164
239	accaccatgt tctctaaciaa cttctatatt ccagctgatc actgcttcag ggcttagatg	1224
240	cctgcttttg ccttcaagtc tccccttaaa gatactccca caggtctact tgggtggcctg	1284
241	cagccactct gaataggaag tttggtctac aatttcccc ctctgctgct caaaaaaaaa	1344
242	aattagtaga tatgattttc ccatattctc cctgccaag taattttttc cagcaagac	1404
243	atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa catttctcag	1464

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:16; Xaa Pos. 6,7,22,24,25,35,43,58,82,84,97,99,107,108,122,130,153,154
Seq#:16; Xaa Pos. 161,163,166,171,198,200
Seq#:17; Xaa Pos. 3,5,9,11,14,16,18,20,21,22,23,25,27,29,30,31,32,33,35,36
Seq#:17; Xaa Pos. 39,40,41,42,43,47,48,50,51,52,53,57,58,63,66,68,69,71,72
Seq#:17; Xaa Pos. 73,74,77,78,81,83,84,86,87,88,89,91,93,100,102,107,108
Seq#:17; Xaa Pos. 109,110,112,113,118,120,127,128,129,130,131,135,139,140
Seq#:17; Xaa Pos. 141,142,146,147,148,150,151,153,155,156,158,159,160,162
Seq#:17; Xaa Pos. 163,166,168,171,173,174,175,176,177,182,184,185,187,190
Seq#:17; Xaa Pos. 192,194,195,197,198,199,200,202,203,207,208,211,212,213
Seq#:17; Xaa Pos. 214
Seq#:23; Xaa Pos. 198,199,200,201,202,203,204,205,206,207,208,209,210,211
Seq#:23; Xaa Pos. 212,213,214,215,216

VERIFICATION SUMMARY

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L:517 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:520 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:554 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:557 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:633 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:636 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:192
M:341 Repeated in SeqNo=23